

In the specification:

[0100] Construction of a biased peptide library has been described previously. Martin et al., *J. Biol. Chem.* 271:361-366, 1996; Schatz et al., *Meth. Enzymol.* 267:171-191, 1996. The vector used for library construction was pJS142 (see Figure 2). This vector had a linker sequence between the LacI and the biased undercamer undecamer peptide coding sequence, as well as restriction sites for cloning the library oligonucleotide. The oligonucleotide synthesized to encode the mutagenesis library was synthesized with 70% of the correct base and 10% of each of the other bases at each position. This mutagenesis rate leads to a biased library such that there is approximately a 50% chance that any of the 11 codons will be the appropriate amino acid and approximately a 50% chance that it will be another amino acid. In addition, a linker of four random NNK (where N denotes A, C, G or T and K denotes G or T) codons were synthesized at the 5' end of the sequence to make a total of 15 randomized codons. Using this method, a library with greater than 10^9 independent clones per microgram of vector used in the ligation was constructed based on the carboxyl terminal sequence of Gat (IKENLKDCGLF; SEQ ID NO:139). The nucleic acid used for creating this library was 5'-GAGGTGGTNNKNNKNNKNNKatacaaggagaacctgaaggactgcggcctttcTAACTAAGTAAAGC-3', wherein N= A/C/G/T and K= G/T; SEQ ID NO:140).